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Nabeela R McMillian Marshall Gerstein & Borun 6300 Sears Tower 233 South Wacker Drive Chicago, IL 60606-6402			EXAMINER	
			CHAKRABARTI, ARUN K	
			ART UNIT	PAPER NUMBER
3.7			1634	
			DATE MAILED: 09/29/2003	

Please find below and/or attached an Office communication concerning this application or proceeding.

# Office Action Summary

Application No.

Applicant(s)

10/018,453

Zabeau

Examiner

Arun Chakrabarti

Art Unit 1634



Period for Reply A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE MONTH(S) FROM					
A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE MONTH(S) FROM					
THE MAILING DATE OF THIS COMMUNICATION.  - Extensions of time may be available under the provisions of 37 CFR 1.136 (a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the					
mailing date of this communication.  If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.					
<ul> <li>If the period for reply is specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered threely.</li> <li>If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.</li> <li>Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).</li> <li>Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).</li> </ul>					
Status					
1) X Responsive to communication(s) filed on Jul 23, 2003	_ •				
2a) X This action is <b>FINAL</b> . 2b) This action is non-final.					
Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under <i>Ex parte Quayle</i> , 1935 C.D. 11; 453 O.G. 213.					
Disposition of Claims					
4) X Claim(s) 57-96, 100, 102, and 104-114 is/are pending in the application.					
4a) Of the above, claim(s) is/are withdrawn from considerations.	tion.				
5) Claim(s) is/are allowed.					
6) X Claim(s) 57-96, 100, 102, and 104-114 is/are rejected.					
7) Claim(s) is/are objected to.					
8) Claims are subject to restriction and/or election require	nent.				
Application Papers					
9) The specification is objected to by the Examiner.					
10) The drawing(s) filed on is/are a) accepted or b) objected to by the Examiner,					
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).					
11) The proposed drawing correction filed on is: a) approved b) disapproved by the Ex	aminer.				
If approved, corrected drawings are required in reply to this Office action.					
12) The oath or declaration is objected to by the Examiner.					
Priority under 35 U.S.C. §§ 119 and 120					
13) Acknowledgement is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).					
a) 🗌 All b) 🗎 Some* c) 🗎 None of:					
1. Certified copies of the priority documents have been received.					
2. Certified copies of the priority documents have been received in Application No					
3. Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).					
*See the attached detailed Office action for a list of the certified copies not received.					
14) Acknowledgement is made of a claim for domestic priority under 35 U.S.C. § 119(e).					
a) The translation of the foreign language provisional application has been received.					
15) Acknowledgement is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.					
Attachment(s)  1) Notice of References Cited (PTO-892)  4) Interview Summary (PTO-413) Paper No(s).					
	Notice of Informal Patent Application (PTO-152)				
3) X Information Disclosure Statement(s) (PTO-1449) Paper No(s). 0803 6) X Other: Detailed Action	i				

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#### **DETAILED ACTION**

### Status of the Application

1. The amendment received on July 23, 2003 has been entered. Claims 57, 61, 84, 89, 92-96, 99, 100, and 102 have been amended. New claims 104-114 have been added. Claims 57-96, 100, 102, and 104-114 are pending in this application.

#### Claim Rejections - 35 USC § 102

2. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

- (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
- 3. Claims 57 and 96 are rejected under 35 U.S.C. 102(b) as being anticipated by Koster (PCT International Publication Number WO 96/29431) (September 26, 1996).

Koster teach a method for sequencing one or more target nucleic acids present in one or more biological samples (Abstract), the method comprising the steps of:

- a) deriving from one or more biological samples the one or more target nucleic acids (Example 5);
- b) subjecting the one or more target nucleic acids obtained from step (a) to two or more separate base-specific, sequence-specific or site-specific complementary cleavage reactions,

wherein each cleavage reaction generates a non-ordered fragments (page 6, lines 8-14 and Figure 7B and 8, and page 24, lines 1-12);

- c) analyzing the sets of non-ordered fragments obtained from step(b) by mass spectrometry (Page 48, line 28 to page 53, line 19 and Figures 8 and 47 A-D); and,
- d) performing a systematic computational analysis on the mass spectra obtained from step c) to analyze the sequence of the target nucleic acid, wherein the complementary cleavage reactions refer to target nucleic acid digestion characterized by varying specificity and/or to digestion of alternative forms of the target sequence (Page 48, line 28 to page 53, line 19).
- 4. Claims 100 and 102 are rejected under 35 U.S.C. 102(b) as being anticipated by New England BioLabs Catalog (Product Number # 203S and 203L, Page 74, 1996-1997).

New England BioLabs Catalog teaches a kit comprising:

a) one or more nucleotide triphosphates (Reaction buffer and Unit assay Conditions Section); b) one or more polymerases; c) one or more nucleic acid cleaving agents (Page 74, T4 DNA polymerase inherently have 3'-5' exonuclease activity as described in Description Section); and d) one or more sets of reference nucleic acids for which the nucleic acid sequence is known (Reaction buffer and Unit assay Conditions Section); e) optionally, reagents to purify the target nucleic acid (Reaction buffer and Unit assay Conditions Section).

New England BioLabs Catalog inherently teaches the use of a kit for analyzing the sequence of known and unknown sequences present in one or more biological samples (Applications Section).

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### Claim Rejections - 35 USC § 103

5. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103© and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

6. Claims 58-71, 73-80, 82-83, 85-91, and 105-107 are rejected under 35 U.S.C. 103(a) over Koster (PCT International Publication Number WO 96/29431) (September 26, 1996) in view of Monforte et al. (PCT International Publication Number WO 97/33000) (September 12, 1997).

Koster teaches the method of claims 57 and 96 as described above.

Koster does not teach the method, wherein the one or more biological samples are derived from organism selected from eukaryotes.

Monforte et al teach a method, wherein the one or more biological samples are derived from organism selected from eukaryotes (Page 16, lines 29-30).

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Koster does not teach the method, wherein the one or more target nucleic acids are selected from single stranded DNA, double stranded DNA, single stranded RNA, double stranded RNA, DNA/RNA hybrid

Monforte et al teach a method, wherein the one or more target nucleic acids are selected from single stranded DNA, double stranded DNA, single stranded RNA, double stranded RNA, DNA/RNA hybrid (Figures 2-13 and Page 32, line 25 to page 36, line 32).

Koster does not teach the method, wherein one or more target nucleic acids are derived by one or more consecutive amplification procedures selected from PCR.

Monforte et al teach a method, wherein one or more target nucleic acids are derived by one or more consecutive amplification procedures selected from PCR (Page 6, lines 1-10, and Column 17, lines 6-8 and Figure 2).

Koster does not teach the method, wherein the derived target nucleic acid incorporates one or more nucleosides that are modified on the base, the sugar, and/or the phosphate moiety, wherein the modifications alter the mass and/or the length of the cleavage products.

Monforte et al teach a method, wherein the derived target nucleic acid incorporates one or more nucleosides that are modified on the base, the sugar, and/or the phosphate moiety, wherein the modifications alter the mass and/or the length of the cleavage products (Page 26, line 5 to page 28, line 2).

Koster does not teach the method, wherein the modification is introduced chemically.

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Monforte et al teach a method, wherein the modification is introduced chemically (Page 27, first paragraph).

Koster does not teach the method, wherein the modification consists of a 2'-deoxy substituent on the nucleoside triphosphates.

Monforte et al teach a method, wherein the modification consists of a 2'-deoxy substituent on the nucleoside triphosphates (Figure 4B and Example 4).

Koster does not teach the method, wherein the modification consists of a methyl group on C5 of the uridine-5'-monophosphate subunits (Example 4) using an alkylating reagent.

Monforte et al teach a method, wherein the modification consists of a methyl group on C5 of the uridine-5'-monophosphate subunits (Example 4) using an alkylating reagent (Figure 4B and Example 4).

Koster does not teach the method, wherein the one or more targets nucleic acids of step(a) are purified prior to cleavage through immobilization.

Monforte et al teach a method, wherein the one or more targets nucleic acids of step(a) are purified prior to cleavage through immobilization (Example 8, page 56, lines 30-34).

Koster does not teach the method, wherein the complementary cleavage reactions are selected from enzymatic (endonucleases and exonucleases) and chemical cleavage (alkali) (Figures 7-8).

Koster does not teach the method, wherein the complementary cleavage reactions are characterized by a mono-nucleotide or di-nucleotide specificity.

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Monforte et al teach a method, wherein the complementary cleavage reactions are characterized by a mono-nucleotide or di-nucleotide specificity (Figures 2-13 and Examples 5-7).

Koster does not teach the method, wherein the one or more target nucleic acids are subjected to enzymatic cleavage reaction using RNA endonuclease RNAse-A.

Monforte et al teach a method, wherein the one or more target nucleic acids are subjected to enzymatic cleavage reaction using RNA endonuclease RNAse-A (Claim 42, and page 33, line 27, and page 37, lines 19-25).

Koster does not teach the method, wherein the one or more target nucleic acids are mosaic RNA/DNA nucleic acids prepared with mutant polymerase.

Monforte et al teach a method, wherein the one or more target nucleic acids are mosaic RNA/DNA nucleic acids prepared with mutant polymerase (Example 1).

Koster does not teach the method, wherein the set of non-ordered fragments of step(b) is additionally purified using an ion exchange beads.

Monforte et al teach a method, wherein the set of non-ordered fragments of step(b) is additionally purified using an ion exchange beads (Example 10).

Koster does not teach the method, wherein the set of non-ordered fragments of step(b) is spotted onto a solid support chosen from solid surfaces or plates.

Monforte et al teach a method, wherein the set of non-ordered fragments of step(b) is spotted onto a solid support chosen from solid surfaces or plates (Examples 9-10, and Claims 19 and 43 and page 46, lines 13-32).

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Koster teaches the method, wherein the mass spectrometric analysis of the nucleic acid fragments is performed using MALDI-TOF (Figures 7-9).

Koster does not teach the method, wherein the reference nucleic acid sequence is known and comprises an additional step wherein the one or more mass spectra of the non-ordered fragments obtained in step c) are compared with the known or predicted mass spectra for a reference nucleic acid sequence, and deducing therefrom, by systematic computational analysis, all or part of the nucleotide sequence of the one or more target nucleic acids, and comparing the deduced nucleic acid sequence with the reference nucleic acid to determine whether the one or more target nucleic acids have the same sequence or a different sequence from the reference nucleic acid.

Monforte et al teach a method, wherein the reference nucleic acid sequence is known and comprises an additional step wherein the one or more mass spectra of the non-ordered fragments obtained in step c) are compared with the known or predicted mass spectra for a reference nucleic acid sequence, and deducing therefrom, by systematic computational analysis, all or part of the nucleotide sequence of the one or more target nucleic acids, and comparing the deduced nucleic acid sequence with the reference nucleic acid to determine whether the one or more target nucleic acids have the same sequence or a different sequence from the reference nucleic acid (Figures 10-18).

Koster does not teach the method, wherein the nucleic acid sequence difference that is determined is a deletion, substitution, insertions or combinations thereof.

Monforte et al teach a method, wherein the nucleic acid sequence difference that is determined is a deletion, substitution, insertions or combinations thereof (Figures 10-11).

Koster does not teach the method, wherein the nucleic acid sequence difference is a Single Nucleotide Polymorphism (SNP).

Monforte et al teach a method, wherein the nucleic acid sequence difference is a Single Nucleotide Polymorphism (SNP) (Figures 3, 4A-B, and 10A and page 27, line 10 to page 28, line 2).

It would have been *prima facie* obvious to one having ordinary skill in the art at the time the invention was made to combine and substitute the detection of SNP of Monforte et al. in the method of sequencing of nucleic acid of Koster, since Monforte et al. state, "This invention relates to methods for screening nucleic acids for mutations by analyzing nonrandomly fragmented nucleic acids using mass spectrometric techniques and to procedures for improving mass resolution and mass accuracy of these methods of detecting mutations (Abstract)." An ordinary practitioner would have been motivated to combine and substitute the detection of SNP of Monforte et al. in the method of sequencing of nucleic acid of Koster, in order to achieve the express advantage, as noted by Monforte et al, of the assays of the invention that relates to methods for screening nucleic acids for mutations by analyzing nonrandomly fragmented nucleic acids using mass spectrometric techniques and to procedures for improving mass resolution and mass accuracy of these methods of detecting mutations.

7. Claim 72 is rejected under 35 U.S.C. 103(a) over Koster (PCT International Publication Number WO 96/29431) (September 26, 1996) in view of Monforte et al. (PCT International Publication Number WO 97/33000) (September 12, 1997) further in view of Geysen et al. (U.S. Patent 6,475,807 B1) (November 5, 2002).

Koster in view of Monforte et al teach the method of claims 57-71, 73-80, 82-83, 85-91, and 96 as described above.

Koster in view of Monforte et al do not teach the method, wherein the modification consists of nucleotides that incorporate alternative isotopes.

Geysen et al. teach the method, wherein the modification consists of nucleotides that incorporate alternative isotopes (Column 9, lines 29-59, and Examples 1-27).

It would have been *prima facie* obvious to one having ordinary skill in the art at the time the invention was made to combine and substitute the modification consisting of nucleotides that incorporate alternative isotopes of Geysen et al. in the method of Koster in view of Monforte et al. since Geysen et al. state, "If a nitrogen atom in such molecule having an atomic weight of 14 (N 14) is replaced by isotope N 15, then the MS peak will shift to the right precisely one unit to 306. Furthermore, such isotopic doping will not affect the ionization or chemical reactivity of the molecule. The ability to measure both of the properties of mass and ionic intensity with reasonable accuracy (i.e., mass to about 0.1 atomic mass units and relative intensity to about 3%) provides the basis for a novel encoding strategy using isotopes to isotopically, rather than chemically, encode a monomer to read a synthetic history, instead of tagging a molecule itself. Using the

methods of the invention, encoding strategies are devised from the use of the mass information alone, the relative intensity information in two or more mass peaks alone or a combination of the two. The basic methodology of the invention, which is to insert different isotopes into combinatorial constructs to identify addition of monomers or chemical conditions, gives rise to several alternative embodiments for encoding and decoding, which are capable of individual implementation or in selected combinations (Column 9, lines 36-55)." An ordinary practitioner would have been motivated to combine and substitute the modification consisting of nucleotides that incorporate alternative isotopes of Geysen et al. in the method of Koster in view of Monforte et al., in order to achieve the express advantage, as noted by Geysen et al, of the assays of the invention which has the ability to measure both of the properties of mass and ionic intensity with reasonable accuracy (i.e., mass to about 0.1 atomic mass units and relative intensity to about 3%) thus providing the basis for a novel encoding strategy using isotopes to isotopically, rather than chemically, encode a monomer to read a synthetic history, instead of tagging a molecule itself and new encoding strategies from the use of the mass information alone, the relative intensity information in two or more mass peaks alone or a combination of the two, which gives rise to several alternative embodiments for encoding and decoding, which are capable of individual implementation or in selected combinations.

8. Claim 81 is rejected under 35 U.S.C. 103(a) over Koster (PCT International Publication Number WO 96/29431) (September 26, 1996) in view of Hanna (U.S. Patent 6,107,039) (August 22, 2000).

Koster teaches the method of claims 57 and 96 as described above.

Koster does not teach the method, wherein the cleavage reactions are performed with the nuclease P1.

Hanna teaches the method, wherein the cleavage reactions are performed with the nuclease P1 (Column 24, lines 5-11).

It would have been *prima facie* obvious to one having ordinary skill in the art at the time the invention was made to combine and substitute the method, wherein the cleavage reactions are performed with the nuclease P1 of Hanna in the method of Koster since Hanna states, "Substitution of the exonuclease SVP with an endonuclease Nuclease P1 resulted in complete digestion (Column 24, lines 5-6)." An ordinary practitioner would have been motivated to combine and substitute the method, wherein the cleavage reactions are performed with the nuclease P1 of Hanna in the method of Koster, in order to achieve the express advantage, as noted by Hanna, of the substitution of the exonuclease SVP with an endonuclease Nuclease P1 that resulted in complete digestion.

9. Claim 84 and 104 is rejected under 35 U.S.C. 103(a) over Koster (PCT International Publication Number WO 96/29431) (September 26, 1996) in view of New England BioLabs Catalog (Product Numbers # 251L and 207L, Page 75, 1996-1997).

Koster teaches the method of claims 57 and 96 as described above.

Koster does not teach the method, wherein the one or more target nucleic acids are RNA/DNA transcripts that incorporate either dCMP, dUMP or dTMP, prepared with mutant T7 or SP6 polymerase.

New England BioLabs Catalog teaches the method, wherein the one or more target nucleic acids are RNA/DNA transcripts that incorporate either dCMP, dUMP or dTMP, prepared with mutant T7 or SP6 polymerase (Product Numbers # 251L and 207L, Page 75, 1996-1997).

It would have been *prima facie* obvious to one having ordinary skill in the art at the time the invention was made to combine and substitute the method, wherein the one or more target nucleic acids are RNA/DNA transcripts that incorporate either dCMP, dUMP or dTMP, prepared with mutant T7 or SP6 polymerase of New England BioLabs Catalog in the method of Koster since BioLab Catalog states, "RNA produced using the T7 and SP6 RNA polymerases is biologically active as mRNA and can be accurately spliced. Anti-sense RNA produced by reversing the orientation of the cloned DNA insert, has been shown to specifically block mRNA translation in vivo. Labeled single-stranded RNA transcripts of high specific activity are simple to prepare with T7 and SP6 RNA polymerases. Increased levels of detection in nucleic acid hybridization reactions can also be obtained due to the greater stability of RNA-DNA hybrids (Column 1, Page 75, Description section)." An ordinary practitioner would have been motivated to combine and substitute the method, wherein the one or more target nucleic acids are RNA/DNA transcripts that incorporate either dCMP, dUMP or dTMP, prepared with mutant T7 or SP6 polymerase of New England BioLabs Catalog in the method of Koster, in order to achieve

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the express advantage, as noted by BioLab Catalog, of mutant T7 and SP6 RNA polymerases which provides the simple preparation of labeled single-stranded RNA transcripts of high specific activity, increased levels of detection in nucleic acid hybridization, and preparation of biologically active mRNA that can be accurately spliced.

10. Claims 108-114 are rejected under 35 U.S.C. 103(a) over New England BioLabs Catalog (Product Number # 203S and 203L, Page 74, 1996-1997) in view of Monforte et al. (PCT International Publication Number WO 97/33000) (September 12, 1997).

New England BioLabs Catalog teaches the kit of claims 100 and 102 as described above.

New England BioLabs Catalog does not teach the kit comprising RNAse T1, reagents to purify the target nucleic acid, ion exchange beads in order to purify the non-ordered set of fragments, a computer software for comparing the mass spectra of the one or more target nucleic acid with the mass spectra of the reference nucleic acid and deducing therefrom the nucleic acid sequence of the target nucleic acid.

Monforte et al. teaches the kit comprising RNAse T1, reagents to purify the target nucleic acid, ion exchange beads in order to purify the non-ordered set of fragments, a solid support suitable for use in mass spectrometry, a computer software for comparing the mass spectra of the one or more target nucleic acid with the mass spectra of the reference nucleic acid and deducing therefrom the nucleic acid sequence of the target nucleic acid (Page 13, line 23 to page 14, line 4 and Claim 42, and page 33, line 27, and page 37, lines 19-25 and Examples 9-10, and Claims 19 and 43 and page 46, lines 13-32 and page 22, lines 3-23).

It would have been *prima facie* obvious to one having ordinary skill in the art at the time the invention was made to combine and substitute the kit for detection of SNP of Monforte et al. in the kit of sequencing of nucleic acid of Koster, since Monforte et al. state, "This invention relates to methods for screening nucleic acids for mutations by analyzing nonrandomly fragmented nucleic acids using mass spectrometric techniques and to procedures for improving mass resolution and mass accuracy of these methods of detecting mutations (Abstract)." An ordinary practitioner would have been motivated to combine and substitute the kit for detection of SNP of Monforte et al. in the kit of sequencing of nucleic acid of Koster, in order to achieve the express advantage, as noted by Monforte et al, of the assays of the invention that relates to methods for screening nucleic acids for mutations by analyzing nonrandomly fragmented nucleic acids using mass spectrometric techniques and to procedures for improving mass resolution and mass accuracy of these methods of detecting mutations.

#### Response to Amendment

11. In response to amendment, rejections under 35 U.S.C. 101 and 112 (second paragraph) have been withdrawn. Previous 102(b) rejection as being anticipated by Monforte has also been withdrawn. However, new 102(b) rejection has been included and previous 102(b) rejection based on New England BioLabs catalog has been properly maintained. Previous 103(a) rejections have been withdrawn. New 103(a) rejections have been included.

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## Response to Arguments

12. Applicant's arguments with respect to all pending claims have been considered but are most in view of the new ground(s) of rejection.

102(b) rejection based on New England BioLabs catalog has been properly maintained because of the following reason. Applicant argues (Page 17, second paragraph) that this rejection should be withdrawn because this cited reference does not teach "a solid support suitable for use in mass spectrometry analysis". This argument is not persuasive. In response to applicant's argument that a support for use in mass spectrometry analysis is not taught by the reference, a recitation of the intended use of the claimed invention must result in a structural difference between the claimed invention and the prior art in order to patentably distinguish the claimed invention from the prior art. If the prior art structure is capable of performing the intended use, then it meets the claim. In a claim drawn to a process of making, the intended use must result in a manipulative difference as compared to the prior art. See *In re Casey*, 152 USPQ 235 (CCPA 1967) and *In re Otto*, 136 USPQ 458, 459 (CCPA 1963). In this case, support suitable for use in mass spectrometry analysis is merely intended use and impose no structural difference from the cited prior art of New England BioLabs catalog, which inherently teaches a solid support.

#### Conclusion

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Applicant's amendment necessitated the new ground(s) of rejection presented in this Office 13. action. Accordingly, THIS ACTION IS MADE FINAL. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Arun Chakrabarti, Ph.D., whose telephone number is (703) 306-5818. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion, can be reached on (703) 308-1119. Any inquiry of a general nature or relating to the status of this application should be directed to the Group analyst Chantae Dessau whose telephone number is (703) 605-1237. Papers related to this application may be submitted to Technology Center 1600 by facsimile transmission via the P.T.O. Fax Center located in Crystal Mall 1. The CM1 Fax Center numbers for Technology Center 1600 are either (703) 746-4979.

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Please note that the faxing of such papers must conform with the Notice to Comply published in

the Official Gazette, 1096 OG 30 (November 15, 1989),

ARUNK CHAKRABARTI

Arun Chakrabarti PATENT EXAMINER

Patent Examiner Art Unit 1634

September 23, 2003

GARY BENZION, PH.D.

UPERVISORY PATENT EXAMER

TECHNOLOGY CENTER 1889